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Sequence Listing was accepted.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)  
217-9197 (toll free).

Reviewer: Keisha Douglas

Timestamp: [year=2008; month=9; day=10; hr=12; min=41; sec=21; ms=61; ]

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Application No: 10587756 Version No: 2.0

Input Set:

Output Set:

```

Started:      2008-08-07 19:48:31.656
Finished:    2008-08-07 19:48:35.857
Elapsed:     0 hr(s) 0 min(s) 4 sec(s) 201 ms
Total Warnings: 3
Total Errors: 36
No. of SeqIDs Defined: 46
Actual SeqID Count: 46

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[illegible]

**Input Set:**

**Output Set:**

**Started:** 2008-08-07 19:48:31.656

**Finished:** 2008-08-07 19:48:35.857

**Elapsed:** 0 hr(s) 0 min(s) 4 sec(s) 201 ms

**Total Warnings:** 3

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**No. of SeqIDs Defined:** 46

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Error code	Error Description
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna This error has occurred more than 20 times, will not be displayed

## SEQUENCE LISTING

<110> Miyake, Masato  
Yoshikawa, Tomohiro  
Mikyake, Jun

## <120> EVENT SEQUENCES

<130> 690121.409USPC

<140> 10587756

<141> 2008-08-07

<150> PCT/JP2005/001151

<151> 2005-01-27

<150> JP 2004-24923

<151> 2004-01-30

<160> 46

<170> PatentIn version 3.1

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<211> 1929

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 $\langle 220 \rangle$ 

<221> CDS

<222> (1) . . (1929)

<223> fibronectin 1

$\langle 400 \rangle$  1

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1 5 10 15

ctg ggg aca gcg gtg ccc tcc acg gga gcc tcg aag agc aag agg cag 96  
Leu Gly Thr Ala Val Pro Ser Thr Gly Ala Ser Lys Ser Lys Arg Gln  
20 25 30

gct cag caa atg gtt cag ccc cag tcc ccg gtg gct gtc agt caa agc 144  
Ala Gln Gln Met Val Gln Pro Gln Ser Pro Val Ala Val Ser Gln Ser  
35 40 45

aag ccc ggt tgt tat gac aat gga aaa cac tat cag ata aat caa cag 192  
Lys Pro Gly Cys Tyr Asp Asn Gly Lys His Tyr Gln Ile Asn Gln Gln  
50 55 60

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 Trp Glu Arg Thr Tyr Leu Gly Asn Ala Leu Val Cys Thr Cys Tyr Gly  
 65 70 75 80

gga agc cga ggt ttt aac tgc gag agt aaa cct gaa gct gaa gag act 288

Gly	Ser	Arg	Gly	Phe	Asn	Cys	Glu	Ser	Lys	Pro	Glu	Ala	Glu	Glu	Thr		
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Cys	Phe	Asp	Lys	Tyr	Thr	Gly	Asn	Thr	Tyr	Arg	Val	Gly	Asp	Thr	Tyr		
			100					105					110				
gag	cgt	cct	aaa	gac	tcc	atg	atc	tgg	gac	tgt	acc	tgc	atc	ggg	gct	384	
Glu	Arg	Pro	Lys	Asp	Ser	Met	Ile	Trp	Asp	Cys	Thr	Cys	Ile	Gly	Ala		
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ggg	cga	ggg	aga	ata	agc	tgt	acc	atc	gca	aac	cgc	tgc	cat	gaa	ggg	432	
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ggt	cag	tcc	tac	aag	att	ggt	gac	acc	tgg	agg	aga	cca	cat	gag	act	480	
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ggt	ggt	tac	atg	tta	gag	tgt	gtg	tgt	ctt	ggt	aat	gga	aaa	gga	gaa	528	
Gly	Gly	Tyr	Met	Leu	Glu	Cys	Val	Cys	Leu	Gly	Asn	Gly	Lys	Gly	Glu		
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Trp	Thr	Cys	Lys	Pro	Ile	Ala	Glu	Lys	Cys	Phe	Asp	His	Ala	Ala	Gly		
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atg	atg	gta	gat	tgt	act	tgc	ctg	gga	gaa	ggc	agc	gga	cgc	atc	act	672	
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tgc	act	tct	aga	aat	aga	tgc	aac	gat	cag	gac	aca	agg	aca	tcc	tat	720	
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cac	acc	tct	gtg	cag	acc	aca	tcg	agc	gga	tct	ggc	ccc	ttc	acc	gat	864	
His	Thr	Ser	Val	Gln	Thr	Thr	Ser	Ser	Gly	Ser	Gly	Pro	Phe	Thr	Asp		
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gtt	cgt	gca	gct	gtt	tac	caa	ccg	cag	cct	cac	ccc	cag	cct	cct	ccc	912	
Val	Arg	Ala	Ala	Val	Tyr	Gln	Pro	Gln	Pro	His	Pro	Gln	Pro	Pro	Pro		
			290				295					300					
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Tyr	Gly	His	Cys	Val	Thr	Asp	Ser	Gly	Val	Val	Tyr	Ser	Val	Gly	Met		

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325		330	335	
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Arg Thr Asp Ser Thr Thr Ser Asn Tyr Glu Gln Asp Gln Lys Tyr Ser				
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Asn Gly Ala Leu Cys His Phe Pro Phe Leu Tyr Asn Asn His Asn Tyr				
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Thr Thr Gln Asn Tyr Asp Ala Asp Gln Lys Phe Gly Phe Cys Pro Met				
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Ala Ala His Glu Glu Ile Cys Thr Thr Asn Glu Gly Val Met Tyr Arg				
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Ile Gly Asp Gln Trp Asp Lys Gln His Asp Met Gly His Met Met Arg				
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Cys Thr Cys Val Gly Asn Gly Arg Gly Glu Trp Thr Cys Ile Ala Tyr				
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tcg cag ctt cga gat cag tgc att gtt gat gac atc act tac aat gtg				1536
Ser Gln Leu Arg Asp Gln Cys Ile Val Asp Asp Ile Thr Tyr Asn Val				
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Asn Asp Thr Phe His Lys Arg His Glu Glu Gly His Met Leu Asn Cys				
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Thr Cys Phe Gly Gln Gly Arg Gly Arg Trp Lys Cys Asp Pro Val Asp				
530		535	540	



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Cys Thr Ser Arg Asn Arg Cys Asn Asp Gln Asp Thr Arg Thr Ser Tyr  
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Arg Ile Gly Asp Thr Trp Ser Lys Lys Asp Asn Arg Gly Asn Leu Leu  
245 250 255

Gln Cys Ile Cys Thr Gly Asn Gly Arg Gly Glu Trp Lys Cys Glu Arg  
260 265 270

His Thr Ser Val Gln Thr Thr Ser Ser Gly Ser Gly Pro Phe Thr Asp  
275 280 285

Val Arg Ala Ala Val Tyr Gln Pro Gln Pro His Pro Gln Pro Pro Pro  
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Tyr Gly His Cys Val Thr Asp Ser Gly Val Val Tyr Ser Val Gly Met  
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Gly Asn Ser Asn Gly Glu Pro Cys Val Leu Pro Phe Thr Tyr Asn Gly  
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Asn Gly Ala Leu Cys His Phe Pro Phe Leu Tyr Asn Asn His Asn Tyr  
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435 440 445

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Ile Gly Asp Gln Trp Asp Lys Gln His Asp Met Gly His Met Met Arg  
465 470 475 480

Cys Thr Cys Val Gly Asn Gly Arg Gly Glu Trp Thr Cys Ile Ala Tyr  
485 490 495

Ser Gln Leu Arg Asp Gln Cys Ile Val Asp Asp Ile Thr Tyr Asn Val  
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515 520 525

Thr Cys Phe Gly Gln Gly Arg Gly Arg Trp Lys Cys Asp Pro Val Asp

530

535

540

Gln Cys Gln Asp Ser Glu Thr Gly Thr Phe Tyr Gln Ile Gly Asp Ser  
 545 550 555 560

Trp Glu Lys Tyr Val His Gly Val Arg Tyr Gln Cys Tyr Cys Tyr Gly  
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Ser Ser Gly Pro Val Glu Val Phe Ile Thr Glu Thr Pro Ser Gln Pro  
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Gly Tyr

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<220>  
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 Ser Leu Ala Asp Gln Glu Ser Cys Lys Gly Arg Cys Thr Gln Gly Phe  
 20 25 30  
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 35 40 45  
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 Ser Cys Cys Ala Asp Tyr Met Glu Gln Cys Lys Pro Gln Val Thr Arg

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65	70	75	80
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Val Glu Glu Pro Lys Asn Asn Thr Asn Thr Gly Val Gln Pro Glu Asn			
	85	90	95
acc tct cca ccc ggt gac cta aat cct cgg acg gac ggc act cta aag			336
Thr Ser Pro Pro Gly Asp Leu Asn Pro Arg Thr Asp Gly Thr Leu Lys			
	100	105	110
ccg aca gcc ttc cta gat cct gag gaa cag cca agc acc cca gcg cct			384
Pro Thr Ala Phe Leu Asp Pro Glu Glu Gln Pro Ser Thr Pro Ala Pro			
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Lys Val Glu Gln Gln Glu Glu Ile Leu Arg Pro Asp Thr Thr Asp Gln			
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	275	280	285

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Gln Glu Glu Cys Glu Gly Ser Ser Leu Ser Ala Val Phe Glu His Phe	
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Ala Leu Leu Gln Arg Asp Ser Trp Glu Asn Ile Phe Glu Leu Leu Phe	
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tgg ggc aga tcc tct gat gga gcc aga gaa ccc caa ttc atc agc cgg	